

SEQUENCE LISTING

<110> McDonald, John R.
Coggins, Philip

<120> METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
OTHER INFLAMMATORY CONDITIONS AND DISORDERS

<130> 25020-601B

<140> Unassigned

<141> 1999-07-22

<160> 70

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> homo sapien

<400> 1

Gly Gly Gly Gly Ser
1 5

<210> 2

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> REPEAT

<222> (1)...(5)

<223> homo sapien

<400> 2

Gly Gly Gly Gly Ser
1 5

<210> 3

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> homo sapien

<400> 3

Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser
1 5 10

<210> 4

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> homo sapien

<400> 4

Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
1 5 10

<210> 5
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 5
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Ser Gly Ser Thr
1 5 10 15
Lys Gly

<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 6
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
1 5 10

<210> 7
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 7
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15
Lys Gly

<210> 8
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 8
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Glu Phe
1 5 10

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 9
Ser Arg Ser Ser Gly
1 5

<210> 10
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 10

Ser Gly Ser Ser Cys
1 5

<210> 11

<211> 28

<212> PRT

<213> diphtheria toxin trypsin sensitive linker

<400> 11

Ala Met Gly Arg Ser Gly Gly Gly Cys Ala Gly Asn Arg Val Gly Ser
1 5 10 15
Ser Leu Ser Cys Gly Gly Leu Asn Leu Gln Ala Met
20 25

<210> 12

<211> 6

<212> PRT

<213> homo sapien

<220>

<221> REPEAT

<222> (3)...(3)

<223> repeat unit 2-4 times

<221> REPEAT

<222> (3)...(4)

<223> repeat family 1-11 times

<400> 12

Ala Met Gly Ser Ala Met
1 5

<210> 13

<211> 74

<212> PRT

<213> homo sapien

<400> 13

Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn Arg
1 5 10 15
Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser Gly
20 25 30
Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys Asp
35 40 45
Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys Tyr
50 55 60
Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro
65 70

<210> 14

<211> 77

<212> PRT

<213> homo sapien

<400> 14

Gly Pro Val Ser Ala Val Leu Thr Glu Leu Arg Cys Thr Cys Leu Arg
1 5 10 15
Val Thr Leu Arg Val Asn Pro Lys Thr Ile Gly Lys Leu Gln Val Phe
20 25 30
Pro Ala Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser Leu Lys
35 40 45

Asn Gly Lys Gln Val Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys Lys
 50 55 60
 Val Ile Gln Lys Ile Leu Asp Ser Gly Asn Lys Lys Asn
 65 70 75

<210> 15
 <211> 127
 <212> PRT
 <213> homo sapien

<400> 15
 Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val
 1 5 10 15
 Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr
 20 25 30
 Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp
 35 40 45
 Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln
 50 55 60
 Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met
 65 70 75 80
 Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys
 85 90 95
 Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp
 100 105 110
 Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 115 120 125

<210> 16
 <211> 73
 <212> PRT
 <213> homo sapien

<400> 16
 Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
 1 5 10 15
 Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser Pro Gly
 20 25 30
 Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Arg
 35 40 45
 Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile Ile Glu
 50 55 60
 Lys Met Leu Asn Ser Asp Lys Ser Asn
 65 70

<210> 17
 <211> 73
 <212> PRT
 <213> homo sapien

<400> 17
 Lys Ser Met Gln Val Pro Phe Ser Arg Cys Cys Phe Ser Phe Ala Glu
 1 5 10 15
 Gln Glu Ile Pro Leu Arg Ala Ile Leu Cys Tyr Arg Asn Thr Ser Ser
 20 25 30
 Ile Cys Ser Asn Glu Gly Leu Ile Phe Lys Leu Lys Arg Gly Lys Glu
 35 40 45
 Ala Cys Ala Leu Asp Thr Val Gly Trp Val Gln Arg His Arg Lys Met
 50 55 60
 Leu Arg His Cys Pro Ser Lys Arg Lys
 65 70

<210> 18
 <211> 133
 <212> PRT

<213> homo sapien

<400> 18
Ala Pro Met Thr Gln Thr Thr Pro Leu Lys Thr Ser Trp Val Asn Cys
1 5 10 15
Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu
20 25 30
Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu
35 40 45
Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala
50 55 60
Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn
65 70 75 80
Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His Pro
85 90 95
Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr
100 105 110
Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu
115 120 125
Ser Leu Ala Ile Phe
130

<210> 19
<211> 77
<212> PRT
<213> homo sapien

<400> 19
Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys
1 5 10 15
Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val
20 25 30
Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys Leu
35 40 45
Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln
50 55 60
Arg Val Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser
65 70 75

<210> 20
<211> 76
<212> PRT
<213> homo sapien

<400> 20
Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe Thr
1 5 10 15
Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile Thr
20 25 30
Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val Ala
35 40 45
Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met
50 55 60
Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr
65 70 75

<210> 21
<211> 76
<212> PRT
<213> homo sapien

<400> 21
Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val Ile
1 5 10 15
Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile Thr
20 25 30
Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly

35 40 45
 Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met
 50 55 60
 Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
 65 70 75

<210> 22
 <211> 76
 <212> PRT
 <213> homo sapien

<400> 22
 Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe Ile
 1 5 10 15
 Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr
 20 25 30
 Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu Asp
 35 40 45
 Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe Met
 50 55 60
 Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu
 65 70 75

<210> 23
 <211> 75
 <212> PRT
 <213> homo sapien

<400> 23
 Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser
 1 5 10 15
 Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr
 20 25 30
 Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys
 35 40 45
 Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln Asn Tyr Met Lys
 50 55 60
 His Leu Gly Arg Lys Ala His Thr Leu Lys Thr
 65 70 75

<210> 24
 <211> 70
 <212> PRT
 <213> homo sapien

<400> 24
 Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr
 1 5 10 15
 Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser
 20 25 30
 Ser Gln Cys Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg
 35 40 45
 Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser
 50 55 60
 Asp Leu Glu Leu Ser Ala
 65 70

<210> 25
 <211> 129
 <212> PRT
 <213> homo sapien

<400> 25
 His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn Ser
 1 5 10 15
 Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp Ile

Phe	Ala	Ala	20	Ser	Lys	Asn	Thr	Thr	25	Glu	Lys	Glu	Thr	Phe	30	Cys	Arg	Ala
Ala	Thr	Val	35	Leu	Arg	Gln	Phe	Tyr	40	Ser	His	His	Glu	Lys	45	Asp	Thr	Arg
Cys	Leu	Gly	50	Ala	Thr	Ala	55	Gln	Gln	Phe	His	Arg	His	Lys	60	Gln	Leu	Ile
Arg	Phe	Leu	65	Lys	Arg	Leu	70	Asp	Arg	Asn	Leu	Trp	Gly	Leu	75	Ala	Gly	Leu
Asn	Ser	Cys	85	Pro	Val	Lys	Glu	Ala	Asn	Gln	Ser	Thr	Leu	Glu	90	Asn	Phe	
Leu	Glu	Arg	100	Leu	Lys	Thr	Ile	Met	105	Arg	Glu	Lys	Tyr	Ser	110	Lys	Cys	Ser
Ser			115						120						125			

<210> 26
 <211> 73
 <212> PRT
 <213> homo sapien

Ala	Pro	Leu	Ala	Thr	Glu	Leu	Arg	Cys	Gln	Cys	Leu	Gln	Thr	Leu	Gln	15
Gly	Ile	His	Leu	Lys	Asn	Ile	Gln	Ser	Val	Lys	Val	Lys	Ser	Pro	Gly	30
Pro	His	Cys	Ala	Gln	Thr	Glu	Val	Ile	Ala	Thr	Leu	Lys	Asn	Gly	Gln	45
Lys	Ala	Cys	Leu	Asn	Pro	Ala	Ser	Pro	Met	Val	Lys	Lys	Ile	Ile	Glu	60
Lys	Met	Leu	Lys	Asn	Gly	Lys	Ser	Asn								70

<210> 27
 <211> 73
 <212> PRT
 <213> homo sapien

Ala	Ser	Val	Val	Thr	Glu	Leu	Arg	Cys	Gln	Cys	Leu	Gln	Thr	Leu	Gln	15
Gly	Ile	His	Leu	Lys	Asn	Ile	Gln	Ser	Val	Asn	Val	Arg	Ser	Pro	Gly	30
Pro	His	Cys	Ala	Gln	Thr	Glu	Val	Ile	Ala	Thr	Leu	Lys	Asn	Gly	Lys	45
Lys	Ala	Cys	Leu	Asn	Pro	Ala	Ser	Pro	Met	Val	Gln	Lys	Ile	Ile	Glu	60
Lys	Ile	Leu	Asn	Lys	Gly	Ser	Thr	Asn								70

<210> 28
 <211> 69
 <212> PRT
 <213> homo sapien

Ala	Gln	Val	Gly	Thr	Asn	Lys	Glu	Leu	Cys	Cys	Leu	Val	Tyr	Thr	Ser	15
Trp	Gln	Ile	Pro	Gln	Lys	Phe	Ile	Val	Asp	Tyr	Ser	Glu	Thr	Ser	Pro	30
Gln	Cys	Pro	Lys	Pro	Gly	Val	Ile	Leu	Leu	Thr	Lys	Arg	Gly	Arg	Gln	45
Ile	Cys	Ala	Asp	Pro	Asn	Lys	Lys	Trp	Val	Gln	Lys	Tyr	Ile	Ser	Asp	60
Leu	Lys	Leu	Asn	Ala												65

<210> 29
 <211> 68
 <212> PRT
 <213> homo sapien

<400> 29
 Ser Pro Tyr Ser Ser Asp Thr Thr Pro Cys Cys Phe Ala Tyr Ile Ala
 1 5 10 15
 Arg Pro Leu Pro Arg Ala His Ile Lys Glu Tyr Phe Tyr Thr Ser Gly
 20 25 30
 Lys Cys Ser Asn Pro Ala Val Val Phe Val Thr Arg Lys Asn Arg Gln
 35 40 45
 Val Cys Ala Asn Pro Glu Lys Lys Trp Val Arg Glu Tyr Ile Asn Ser
 50 55 60
 Leu Glu Met Ser
 65

<210> 30
 <211> 69
 <212> PRT
 <213> homo sapien

<400> 30
 Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys Phe Ser Tyr Thr
 1 5 10 15
 Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr Tyr Glu Thr Ser
 20 25 30
 Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr Lys Arg Ser Lys
 35 40 45
 Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln Glu Tyr Val Tyr
 50 55 60
 Asp Leu Glu Leu Asn
 65

<210> 31
 <211> 323
 <212> PRT
 <213> homo sapien

<400> 31
 Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg Glu Ser
 1 5 10 15
 Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu Lys Ala
 20 25 30
 Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp
 35 40 45
 Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu
 50 55 60
 Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn
 65 70 75 80
 Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala
 85 90 95
 Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu
 100 105 110
 Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly
 115 120 125
 Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His
 130 135 140
 His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser
 145 150 155 160
 Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser
 165 170 175
 Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu
 180 185 190
 Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser
 195 200 205

His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile
 210 215 220
 Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu
 225 230 235 240
 Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys
 245 250 255
 His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg
 260 265 270
 His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu
 275 280 285
 Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val
 290 295 300
 Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His
 305 310 315 320
 Asn Glu Leu

<210> 32
 <211> 74
 <212> PRT
 <213> homo sapien

<400> 32
 Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe
 1 5 10 15
 Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn
 20 25 30
 Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn
 35 40 45
 Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu
 50 55 60
 Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
 65 70

<210> 33
 <211> 71
 <212> PRT
 <213> homo sapien

<400> 33
 Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys Leu Glu Tyr Phe Lys
 1 5 10 15
 Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp Tyr Gln Thr Ser Glu
 20 25 30
 Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr Val Gln Gly Arg Ala
 35 40 45
 Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys Asn Ala Val Lys Tyr
 50 55 60
 Leu Gln Ser Leu Glu Arg Ser
 65 70

<210> 34
 <211> 247
 <212> PRT
 <213> Bryonia dioica

<400> 34
 Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Thr Thr Ser Tyr Gly Val
 1 5 10 15
 Phe Ile Lys Asn Leu Arg Glu Ala Leu Pro Tyr Glu Arg Lys Val Tyr
 20 25 30
 Asn Ile Pro Leu Leu Arg Ser Ser Ile Ser Gly Ser Gly Arg Tyr Thr
 35 40 45
 Leu Leu His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Val
 50 55 60
 Asp Val Thr Asn Val Tyr Ile Met Gly Tyr Leu Ala Gly Asp Val Ser
 65 70 75 80

Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Phe Val Phe
 85 90 95
 Lys Asp Ala Lys Lys Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
 100 105 110
 Arg Leu Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu Gly
 115 120 125
 Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Tyr Tyr Tyr Thr Ala
 130 135 140
 Ser Ser Ala Ala Ser Ala Leu Leu Val Leu Ile Gln Ser Thr Ala Glu
 145 150 155 160
 Ser Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp
 165 170 175
 Lys Thr Phe Leu Pro Ser Leu Ala Thr Ile Ser Leu Glu Asn Asn Trp
 180 185 190
 Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
 195 200 205
 Phe Glu Ser Pro Val Val Leu Ile Asp Gly Asn Asn Gln Arg Val Ser
 210 215 220
 Ile Thr Asn Ala Ser Ala Arg Val Val Thr Ser Asn Ile Ala Leu Leu
 225 230 235 240
 Leu Asn Arg Asn Asn Ile Ala
 245

<210> 35
 <211> 275
 <212> PRT
 <213> Saponaria officinalis

<400> 35
 Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr
 1 5 10 15
 Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu
 20 25 30
 Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu
 35 40 45
 Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu
 50 55 60
 Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp
 65 70 75 80
 Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser
 85 90 95
 Ala Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys
 100 105 110
 Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln
 115 120 125
 Ile Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp
 130 135 140
 Leu Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val
 145 150 155 160
 Lys Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu
 165 170 175
 Ala Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro
 180 185 190
 Asn Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp
 195 200 205
 Lys Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe
 210 215 220
 Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp
 225 230 235 240
 Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys Ser Ser Asn
 245 250 255
 Glu Ala Asn Ser Thr Val Arg His Tyr Gly Pro Leu Lys Pro Thr Leu
 260 265 270
 Leu Ile Thr
 275

<210> 36

<211> 250
 <212> PRT
 <213> Momordica charantia

<400> 36
 Ala Pro Thr Leu Glu Thr Ile Ala Ser Leu Asp Leu Asn Asn Pro Thr
 1 5 10 15
 Thr Tyr Leu Ser Phe Ile Thr Asn Ile Arg Thr Lys Val Ala Asp Lys
 20 25 30
 Thr Glu Gln Cys Thr Ile Gln Lys Ile Ser Lys Thr Phe Thr Gln Arg
 35 40 45
 Tyr Ser Tyr Ile Asp Leu Ile Val Ser Ser Thr Gln Lys Ile Thr Leu
 50 55 60
 Ala Ile Asp Met Ala Asp Leu Tyr Val Leu Gly Tyr Ser Asp Ile Ala
 65 70 75 80
 Asn Asn Lys Gly Arg Ala Phe Phe Phe Lys Asp Val Thr Glu Ala Val
 85 90 95
 Ala Asn Asn Phe Phe Pro Gly Ala Thr Gly Thr Asn Arg Ile Lys Leu
 100 105 110
 Thr Phe Thr Gly Ser Tyr Gly Asp Leu Glu Lys Asn Gly Gly Leu Arg
 115 120 125
 Lys Asp Asn Pro Leu Gly Ile Phe Arg Leu Glu Asn Ser Ile Val Asn
 130 135 140
 Ile Tyr Gly Lys Ala Gly Asp Val Lys Lys Gln Ala Lys Phe Phe Leu
 145 150 155 160
 Leu Ala Ile Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Ser
 165 170 175
 Asp Lys Ile Pro Ser Glu Lys Tyr Glu Glu Val Thr Val Asp Glu Tyr
 180 185 190
 Met Thr Ala Leu Glu Asn Asn Trp Ala Lys Leu Ser Thr Ala Val Tyr
 195 200 205
 Asn Ser Lys Pro Ser Thr Thr Thr Ala Thr Lys Cys Gln Leu Ala Thr
 210 215 220
 Ser Pro Val Thr Ile Ser Pro Trp Ile Phe Lys Thr Val Glu Glu Ile
 225 230 235 240
 Lys Leu Val Met Gly Leu Leu Lys Ser Ser
 245 250

<210> 37
 <211> 293
 <212> PRT
 <213> Shigella dysenteriae

<400> 37
 Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser
 1 5 10 15
 Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser
 20 25 30
 Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn
 35 40 45
 Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe
 50 55 60
 Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly
 65 70 75 80
 Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser
 85 90 95
 His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser
 100 105 110
 Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met
 115 120 125
 Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser
 130 135 140
 His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg
 145 150 155 160
 Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg
 165 170 175
 Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met

Thr	Ala	Glu	180	Asp	Val	Asp	Leu	Thr	185	Leu	Asn	Trp	Gly	Arg	190	Leu	Ser	Ser
		195						200						205				
Val	Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile			
	210					215							220					
Ser	Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu			
225					230					235					240			
Asn	Cys	His	His	His	Ala	Ser	Arg	Val	Ala	Arg	Met	Ala	Ser	Asp	Glu			
				245					250					255				
Phe	Pro	Ser	Met	Cys	Pro	Ala	Asp	Gly	Arg	Val	Arg	Gly	Ile	Thr	His			
			260					265					270					
Asn	Lys	Ile	Leu	Trp	Asp	Ser	Ser	Thr	Leu	Gly	Ala	Ile	Leu	Met	Arg			
		275					280					285						
Arg	Thr	Ile	Ser	Ser														
	290																	

<210> 38
 <211> 319
 <212> PRT
 <213> Escherichia coli

<400>	38																	
Met	Lys	Cys	Ile	Leu	Phe	Lys	Trp	Val	Leu	Cys	Leu	Leu	Leu	Gly	Phe			
	1			5					10					15				
Ser	Ser	Val	Ser	Tyr	Ser	Arg	Glu	Phe	Thr	Ile	Asp	Phe	Ser	Thr	Gln			
		20						25					30					
Gln	Ser	Tyr	Val	Ser	Ser	Leu	Asn	Ser	Ile	Arg	Thr	Glu	Ile	Ser	Thr			
		35					40					45						
Pro	Leu	Glu	His	Ile	Ser	Gln	Gly	Thr	Thr	Ser	Val	Ser	Val	Ile	Asn			
	50					55					60							
His	Thr	Pro	Pro	Gly	Ser	Tyr	Phe	Ala	Val	Asp	Ile	Arg	Gly	Leu	Asp			
65				70					75					80				
Val	Tyr	Gln	Ala	Arg	Phe	Asp	His	Leu	Arg	Leu	Ile	Ile	Glu	Gln	Asn			
			85					90					95					
Asn	Leu	Tyr	Val	Ala	Gly	Phe	Val	Asn	Thr	Ala	Thr	Asn	Thr	Phe	Tyr			
			100					105					110					
Arg	Phe	Ser	Asp	Phe	Thr	His	Ile	Ser	Val	Pro	Gly	Val	Thr	Thr	Val			
		115					120					125						
Ser	Met	Thr	Thr	Asp	Ser	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Ala			
	130					135					140							
Leu	Glu	Arg	Ser	Gly	Met	Gln	Ile	Ser	Arg	His	Ser	Leu	Val	Ser	Ser			
					150					155					160			
Tyr	Leu	Ala	Leu	Met	Glu	Phe	Ser	Gly	Asn	Thr	Met	Thr	Arg	Asp	Ala			
			165					170						175				
Ser	Arg	Ala	Val	Leu	Arg	Phe	Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg			
			180					185					190					
Phe	Arg	Gln	Ile	Gln	Arg	Glu	Phe	Arg	Gln	Ala	Leu	Ser	Glu	Thr	Ala			
		195					200					205						
Pro	Val	Tyr	Thr	Met	Thr	Pro	Gly	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp			
	210					215					220							
Gly	Arg	Ile	Ser	Asn	Val	Leu	Pro	Glu	Tyr	Arg	Gly	Glu	Asp	Gly	Val			
225					230					235					240			
Arg	Val	Gly	Arg	Ile	Ser	Phe	Asn	Asn	Ile	Ser	Ala	Ile	Leu	Gly	Thr			
				245					250				255					
Val	Ala	Val	Ile	Leu	Asn	Cys	His	His	Gln	Gly	Ala	Arg	Ser	Val	Arg			
			260					265					270					
Ala	Val	Asn	Glu	Glu	Ser	Gln	Pro	Glu	Cys	Gln	Ile	Thr	Gly	Asp	Arg			
		275					280					285						
Pro	Val	Ile	Lys	Ile	Asn	Asn	Thr	Leu	Trp	Glu	Ser	Asn	Thr	Ala	Ala			
	290					295					300							
Ala	Phe	Leu	Asn	Arg	Lys	Ser	Gln	Phe	Leu	Tyr	Thr	Thr	Gly	Lys				
					310					315								
305																		

<210> 39
 <211> 247
 <212> PRT
 <213> Trichosanthews kirilowii

<400> 39
 Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
 1 5 10 15
 Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
 20 25 30
 Asp Ile Pro Leu Leu Arg Ser Ser Leu Pro Gly Ser Gln Arg Tyr Ala
 35 40 45
 Leu Ile His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Ile
 50 55 60
 Asp Val Thr Asn Val Tyr Ile Met Gly Tyr Arg Ala Gly Asp Thr Ser
 65 70 75 80
 Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
 85 90 95
 Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
 100 105 110
 Arg Leu Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu Gly
 115 120 125
 Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
 130 135 140
 Asn Ser Ala Ala Ser Ala Leu Met Val Leu Ile Gln Ser Thr Ser Glu
 145 150 155 160
 Ala Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp
 165 170 175
 Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
 180 185 190
 Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
 195 200 205
 Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
 210 215 220
 Ile Thr Asn Val Asp Ala Gly Val Val Thr Ser Asn Ile Ala Leu Leu
 225 230 235 240
 Leu Asn Arg Asn Asn Met Ala
 245

<210> 40
 <211> 88
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapien His-Tag leader sequence

<400> 40

aaggagatatacc atg ggc agc agc cat cat cat cat cat cac agc agc
 Met Gly Ser Ser His His His His His His Ser Ser
 1 5 10

43

ggc ctg gtg ccg cgc ggc agc cat atg ctc gag gat ccg
 Gly Leu Val Pro Arg Gly Ser His Met Leu Glu Asp Pro
 15 20 25

82

<210> 41
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapien forward primer (Eotaxin)

<400> 41

gggtaatagc atatggggcc agcttctgtc ccaacca

37

<210> 42
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien reverse primer (Eotaxin)

<400> 42

cccgaattct ttcatcgctg gctttggagt tggagatttt tggc

44

<210> 43
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien forward primer (MCP-1)

<400> 43

gggtaatagc atatgcagcc agatgcaatc aatgccccca

39

<210> 44
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien reverse primer (MCP-1)

<400> 44

cccgaattct ttcatcgagc tcttcggagt ttgggtttct t

41

<210> 45
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien forward primer (MCP-3)

<400> 45

catatgcaac cggtaggcat caacacg

27

<210> 46
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien reverse primer (MCP-3)

<400> 46

cactagtaac catcgcaagc ttcggggtct gag

33

<210> 47
<211> 38

<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien forward primer (SDF-1■)

<400> 47
gggtaatagc atatgaagcc cgtcagcctg agctacag

38

<210> 48
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien reverse primer (SDF-1■)

<400> 48
cccgaattct ttcacgcgcca tcttgaacct cttgttttaa gctttc

46

<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Shigella dysenteriae forward primer (Shiga)

<400> 49
gggtaatagc atatgaaaga attcaccctg gacttttcc

39

<210> 50
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Shigella dysenteriae reverse primer (Shiga)

<400> 50
cccgatcca ctagtattaa gcgtgggtg

28

<210> 51
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Shigella dysenteriae reverse primer (Shiga-His6)

<400> 51
cccgatcca ctagtttaat gatgatgggtg gtgggtggcaa ttgag

45

<210> 52
<211> 978
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) .. (978)

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-
toxin fusion protein MCP1-AM-truncated Shiga-A1 Subunit

```

<400> 52
atg cag cca gat gca atc aat gcc cca gtc acc tgc tgt tat aac ttc 48
Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe
1 5 10 15

acc aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc 96
Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile
20 25 30

acc agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg 144
Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val
35 40 45

gcc aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc 192
Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser
50 55 60

atg gac cac ctg gac aag caa acc caa act ccg aag act gcg atg aaa 240
Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Lys
65 70 75 80

gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg 288
Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu
85 90 95

aat gtg att cgt tcc gcg atc ggt acg ccg ctg caa acg att tcc agc 336
Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser
100 105 110

ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg 384
Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu
115 120 125

ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat 432
Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn
130 135 140

aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt 480
Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe
145 150 155 160

gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac 528
Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His
165 170 175

gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct 576
Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser
180 185 190

tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa 624
Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln
195 200 205

atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat 672
Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His
210 215 220

tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc 720
Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe
225 230 235 240

gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc 768

```

Leu Arg Phe Arg Gln Ile Gln Arg Gly
 250 255
 ctg tct ggc cgc agc tat gtg atg act 816
 Leu Ser Gly Arg Ser Tyr Val Met Thr
 265 270
 ctg aac tgg ggt cgc ttg tct tcc gtt 864
 Leu Asn Trp Gly Arg Leu Ser Ser Val
 280 285
 gat tct gtc cgt gtt ggc cgt atc agc 912
 Asp Ser Val Arg Val Gly Arg Ile Ser
 300
 cta ggc tcc gtc gca ctg att ctc aat 960
 Leu Gly Ser Val Ala Leu Ile Leu Asn
 315 320
 978

cial Sequence: Construct encoding chemokine-
 -truncated Shiga-A1 Subunit HIS6

gcc cca gtc acc tgc tgt tat aac ttc 48
 Ala Pro Val Thr Cys Cys Tyr Asn Phe
 10 15
 cag agg ctc gcg agc tat aga aga atc 96
 Gln Arg Leu Ala Ser Tyr Arg Arg Ile
 25 30
 a gaa gct gtg atc ttc aag acc att gtg 144
 s Glu Ala Val Ile Phe Lys Thr Ile Val
 40 45
 c ccc aag cag aag tgg gtt cag gat tcc 192
 p Pro Lys Gln Lys Trp Val Gln Asp Ser
 5 60
 a acc caa act ccg aag act gcg atg aaa 240
 n Thr Gln Thr Pro Lys Thr Ala Met Lys
 75 80
 c act gca aaa act tac gtc gat agc ctg 288
 r Thr Ala Lys Thr Tyr Val Asp Ser Leu
 90 95
 c ggt acg ccg ctg caa acg att tcc agc 336
 e Gly Thr Pro Leu Gln Thr Ile Ser Ser

100	105	110	
ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu 115 120 125			384
ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn 130 135 140			432
aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe 145 150 155 160			480
gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His 165 170 175			528
gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser 180 185 190			576
tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln 195 200 205			624
atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His 210 215 220			672
tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe 225 230 235 240			720
gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly 245 250 255			768
ttc cgc acc act tta gac gat ctg tct ggc cgc agc tat gtg atg act Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr 260 265 270			816
gcc gaa gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val 275 280 285			864
ctg ccg gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt atc agc Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser 290 295 300			912
ttt ggc tct att aat gcc atc cta ggc tcc gtc gca ctg att ctc aat Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn 305 310 315 320			960
tgc cac cac cac cat cat cat taa Cys His His His His His His 325			984

<210> 54
 <211> 999
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) .. (999)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP1-AM-SAPORIN

<400> 54
 atg cag cca gat gca atc aat gcc cca gtc acc tgc tgt tat aac ttc 48
 Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe
 1 5 10 15

acc aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc 96
 Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile
 20 25 30

acc agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg 144
 Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val
 35 40 45

gcc aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc 192
 Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser
 50 55 60

atg gac cac ctg gac aag caa acc caa act ccg aag act gcg atg gtt 240
 Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Val
 65 70 75 80

act agt att acc ctg gac ctg gtc aat ccg acc gcc ggc caa tat agc 288
 Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser
 85 90 95

agc ttc gtg gat aag att cgt aac aac gta aaa gat ccg aat ctg aaa 336
 Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys
 100 105 110

tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa gaa aag 384
 Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys
 115 120 125

ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct ctg ggc 432
 Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly
 130 135 140

ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg gat aat 480
 Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn
 145 150 155 160

acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg agc gcg 528
 Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala
 165 170 175

gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa aaa gca 576
 Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala
 180 185 190

ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg cag atc 624
 Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile
 195 200 205

acc cag ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg 672
 Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu
 210 215 220

ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa 720
 Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys
 225 230 235 240

gac gaa gcc cgc ttc ctg ctg atc gcc att cag atg acg gca gaa gcc	768
Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala	
245 250 255	
gcc cgt ttc cgc tac att cag aac ctg gtc atc aaa aac ttc ccg aac	816
Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn	
260 265 270	
aag ttc aat tcc gag aat aaa gtc att cag ttc gag gtt aat tgg aaa	864
Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys	
275 280 285	
aaa att tcc acc gcc att tat ggt gac gcg aag aac ggt gtt ttc aat	912
Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn	
290 295 300	
aaa gat tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa gac ctg	960
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu	
305 310 315 320	
caa atg ggt ctg ctg atg tac cta gga aaa ccg aag taa	999
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	
325 330	
325 330	

<210> 55
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(978)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP3-AM-truncated Shiga-A1 Subunit

<400> 55	
atg caa ccg gta ggc atc aac acg tcg acc acg tgc tgt tat cgc ttt	48
Met Gln Pro Val Gly Ile Asn Thr Ser Thr Cys Cys Tyr Arg Phe	
1 5 10 15	
atc aac aag aaa atc ccg aaa caa cgc ctg gaa tcc tat cgt cgc acc	96
Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr	
20 25 30	
act agc agc cac tgt ccg cgc gaa gca gtc atc ttc aaa acc aag ctc	144
Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu	
35 40 45	
gat aag gaa atc tgt gca gac ccg act cag aaa tgg gtg caa gat ttt	192
Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe	
50 55 60	
atg aaa cat ctg gat aag aaa act cag acc ccg aag ctt gcg atg aaa	240
Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu Ala Met Lys	
65 70 75 80	
gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg	288
Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu	
85 90 95	

aat	gtg	att	cgt	tcc	gcg	atc	ggg	acg	ccg	ctg	caa	acg	att	tcc	agc	336
Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	
			100					105					110			
ggg	ggg	act	tcc	ctc	ctg	atg	att	gat	tcc	ggg	acg	ggg	gat	aac	ttg	384
Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	
		115					120					125				
ttt	gct	gtt	gat	gtg	cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	ttt	aat	432
Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	
	130					135					140					
aat	ctg	cgt	ctg	atc	gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	ggg	ttt	480
Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	
	145				150					155					160	
gtg	aac	cgt	acg	aac	aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	tcc	cac	528
Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His	
				165					170					175		
gta	acg	ttt	ccg	ggc	acc	act	gct	gtt	act	ctg	agc	ggc	gat	tct	tct	576
Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser	
			180					185					190			
tat	act	acg	tta	cag	cgt	gtg	gct	ggg	atc	agc	cgc	act	ggg	atg	caa	624
Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln	
		195					200					205				
atc	aat	cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	agc	cat	672
Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	
	210					215					220					
tct	ggc	acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	cgc	ttc	720
Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe	
	225				230					235					240	
gtg	acg	gtc	acc	gcc	gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	cgc	ggc	768
Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly	
				245					250					255		
ttc	cgc	acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	816
Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	
			260					265					270			
gcc	gaa	gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggg	cgc	ttg	tct	tcc	gtt	864
Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	
		275					280					285				
ctg	ccg	gat	tat	cac	ggg	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	912
Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	
	290					295					300					
ttt	ggc	tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	960
Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	
	305				310					315					320	
tgc	cac	cac	cac	gct	taa											978
Cys	His	His	His	Ala												
				325												

<210> 56
 <211> 984
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS

<222> (1) .. (984)

<220>

<223> Description of Artificial Sequence: ce: Construct encoding chemokine-toxin fusion protein MCP3-AM-truncated Shiga-A1 subunit HIS6

<400> 56

atg	caa	ccg	gta	ggc	atc	aac	acg	tcg	acc	acg	tgc	tgt	tat	cgc	ttt	48
Met	Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe	
1				5					10					15		
atc	aac	aag	aaa	atc	ccg	aaa	caa	cgc	ctg	gaa	tcc	tat	cgt	cgc	acc	96
Ile	Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr	
			20					25					30			
act	agc	agc	cac	tgt	ccg	cgc	gaa	gca	gtc	atc	ttc	aaa	acc	aag	ctc	144
Thr	Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	
			35				40					45				
gat	aag	gaa	atc	tgt	gca	gac	ccg	act	cag	aaa	tgg	gtg	caa	gat	ttt	192
Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe	
	50					55					60					
atg	aaa	cat	ctg	gat	aag	aaa	act	cag	acc	ccg	aag	ctt	gcg	atg	aaa	240
Met	Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu	Ala	Met	Lys	
65					70					75					80	
gaa	ttc	acc	ctg	gac	ttt	tcc	act	gca	aaa	act	tac	gtc	gat	agc	ctg	288
Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser	Leu	
				85					90					95		
aat	gtg	att	cgt	tcc	gcg	atc	ggc	acg	ccg	ctg	caa	acg	att	tcc	agc	336
Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	
			100				105						110			
ggc	ggc	act	tcc	ctc	ctg	atg	att	gat	tcc	ggc	acg	ggc	gat	aac	ttg	384
Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	
		115					120					125				
ttt	gct	gtt	gat	gtg	cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	ttt	aat	432
Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	
	130					135					140					
aat	ctg	cgt	ctg	atc	gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	ggc	ttt	480
Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	
145					150					155					160	
gtg	aac	cgt	acg	aac	aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	tcc	cac	528
Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His	
				165					170					175		
gta	acg	ttt	ccg	ggc	acc	act	gct	gtt	act	ctg	agc	ggc	gat	tct	tct	576
Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser	
			180					185					190			
tat	act	acg	tta	cag	cgt	gtg	gct	ggc	atc	agc	cgc	act	ggc	atg	caa	624
Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln	
			195				200					205				
atc	aat	cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	agc	cat	672
Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	
	210					215					220					
tct	ggc	acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	cgc	ttc	720
Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe	
225					230					235					240	

gtg	acg	gtc	acc	gcc	gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	cgc	ggc	768
Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly	
				245					250					255		
ttc	cgc	acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	816
Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	
			260					265					270			
gcc	gaa	gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggc	cgc	ttg	tct	tcc	ggt	864
Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	
		275					280					285				
ctg	ccg	gat	tat	cac	ggc	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	912
Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	
		290				295					300					
ttt	ggc	tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	960
Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	
305					310					315					320	
tgc	cac	cac	cac	cat	cat	cat	taa									984
Cys	His	His	His	His	His	His	His									
				325												

<210> 57
 <211> 999
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(999)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin Fusion Protein MCP3-AM-SAPORIN

<400> 57

atg	caa	ccg	gta	ggc	atc	aac	acg	tcc	acc	acg	tgc	tgt	tat	cgc	ttt	48
Met	Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe	
1				5				10						15		
atc	aac	aag	aaa	atc	ccg	aaa	caa	cgc	ctg	gaa	tcc	tat	cgt	cgc	acc	96
Ile	Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr	
			20					25					30			
act	agc	agc	cac	tgt	ccg	cgc	gaa	gca	gtc	atc	ttc	aaa	acc	aag	ctc	144
Thr	Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	
		35				40						45				
gat	aag	gaa	atc	tgt	gca	gac	ccg	act	cag	aaa	tgg	gtg	caa	gat	ttt	192
Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe	
	50					55					60					
atg	aaa	cat	ctg	gat	aag	aaa	act	cag	acc	ccg	aag	ctt	gcg	atg	gtt	240
Met	Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu	Ala	Met	Val	
65					70					75					80	
act	agt	att	acc	ctg	gac	ctg	gtc	aat	ccg	acc	gcc	ggc	caa	tat	agc	288
Thr	Ser	Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	
				85					90					95		
agc	ttc	gtg	gat	aag	att	cgt	aac	aac	gta	aaa	gat	ccg	aat	ctg	aaa	336
Ser	Phe	Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	

100	105	110	
tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa gaa aag			384
Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys			
115	120	125	
ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct ctg ggc			432
Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly			
130	135	140	
ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg gat aat			480
Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn			
145	150	155	160
acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg agc gcg			528
Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala			
	165	170	175
gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa aaa gca			576
Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala			
	180	185	190
ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg cag atc			624
Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile			
	195	200	205
acc cag ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg			672
Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu			
	210	215	220
ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa			720
Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys			
225	230	235	240
gac gaa gcc cgc ttc ctg ctg atc gcc att cag atg acg gca gaa gcc			768
Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala			
	245	250	255
gcc cgt ttc cgc tac att cag aac ctg gtc atc aaa aac ttc ccg aac			816
Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn			
	260	265	270
aag ttc aat tcc gag aat aaa gtc att cag ttc gag gtt aat tgg aaa			864
Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys			
	275	280	285
aaa att tcc acc gcc att tat ggt gac gcg aag aac ggt gtt ttc aat			912
Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn			
	290	295	300
aaa gat tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa gac ctg			960
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu			
305	310	315	320
caa atg ggt ctg ctg atg tac cta gga aaa ccg aag taa			999
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys			
	325	330	

<210> 58
 <211> 963
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF1-AM-truncated Shiga-A1 Subunit

<220>
 <221> CDS
 <222> (1) .. (963)

<400> 58
 aag ccc gtc agc ctg agc tac aga tgc cca tgc cga ttc ttc gaa agc 48
 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1 5 10 15

cat gtt gcc aga gcc aac gtc aag cat ctc aaa att ctc aac act cca 96
 His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
 20 25 30

aac tgt gcc ctt cag att gta gcc cgg ctg aag aac aac aac aga caa 144
 Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
 35 40 45

gtg tgc att gac ccg aag cta aag tgg att cag gag tac ctg gag aaa 192
 Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
 50 55 60

gct tta aac aag agg ttc aag atg gcg atg aaa gaa ttc acc ctg gac 240
 Ala Leu Asn Lys Arg Phe Lys Met Ala Met Lys Glu Phe Thr Leu Asp
 65 70 75 80

ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg att cgt tcc 288
 Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser
 85 90 95

gcg atc ggt acg ccg ctg caa acg att tcc agc ggt ggt act tcc ctc 336
 Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly Thr Ser Leu
 100 105 110

ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct gtt gat gtg 384
 Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala Val Asp Val
 115 120 125

cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg cgt ctg atc 432
 Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile
 130 135 140

gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac cgt acg aac 480
 Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn
 145 150 155 160

aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg ttt ccg ggc 528
 Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly
 165 170 175

acc act gct gtt act ctg agc ggc gat tct tct tat act acg tta cag 576
 Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln
 180 185 190

cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat cgc cat tct 624
 Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser
 195 200 205

ctg acg acc agc tat ctg gac tta atg agc cat tct ggc acc agc ctg 672
 Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu
 210 215 220

acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg gtc acc gcc 720
 Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala
 225 230 235 240

gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc acc act tta	768
Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu	
245 250 255	
gac gat ctg tct ggc cgc agc tat gtg atg act gcc gaa gat gtc gat	816
Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp	
260 265 270	
ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt ctg ccg gat tat cac	864
Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His	
275 280 285	
ggt cag gat tct gtc cgt gtt ggc cgt atc agc ttt ggc tct att aat	912
Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn	
290 295 300	
gcc atc cta ggc tcc gtc gca ctg att ctc aat tgc cac cac cac gct	960
Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His His His Ala	
305 310 315 320	
taa	963

<210> 59

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF1-AM-truncated Shiga-A1 Subunit HIS6

<220>

<221> CDS

<222> (1) .. (969)

<400> 59

aag ccc gtc agc ctg agc tac aga tgc cca tgc cga ttc ttc gaa agc	48
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser	
1 5 10 15	
cat gtt gcc aga gcc aac gtc aag cat ctc aaa att ctc aac act cca	96
His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro	
20 25 30	
aac tgt gcc ctt cag att gta gcc cgg ctg aag aac aac aac aga caa	144
Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln	
35 40 45	
gtg tgc att gac ccg aag cta aag tgg att cag gag tac ctg gag aaa	192
Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys	
50 55 60	
gct tta aac aag agg ttc aag atg gcg atg aaa gaa ttc acc ctg gac	240
Ala Leu Asn Lys Arg Phe Lys Met Ala Met Lys Glu Phe Thr Leu Asp	
65 70 75 80	
ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg att cgt tcc	288
Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser	
85 90 95	
gcg atc ggt acg ccg ctg caa acg att tcc agc ggt ggt act tcc ctc	336
Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly Thr Ser Leu	
100 105 110	

ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct gtt gat gtg	384
Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala Val Asp Val	
115 120 125	
cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg cgt ctg atc	432
Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile	
130 135 140	
gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac cgt acg aac	480
Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn	
145 150 155 160	
aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg ttt ccg ggc	528
Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly	
165 170 175	
acc act gct gtt act ctg agc ggc gat tct tct tat act acg tta cag	576
Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln	
180 185 190	
cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat cgc cat tct	624
Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser	
195 200 205	
ctg acg acc agc tat ctg gac tta atg agc cat tct ggc acc agc ctg	672
Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu	
210 215 220	
acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg gtc acc gcc	720
Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala	
225 230 235 240	
gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc acc act tta	768
Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu	
245 250 255	
gac gat ctg tct ggc cgc agc tat gtg atg act gcc gaa gat gtc gat	816
Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp	
260 265 270	
ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt ctg ccg gat tat cac	864
Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His	
275 280 285	
ggt cag gat tct gtc cgt gtt ggc cgt atc agc ttt ggc tct att aat	912
Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn	
290 295 300	
gcc atc cta ggc tcc gtc gca ctg att ctc aat tgc cac cac cac cat	960
Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His His His His	
305 310 315 320	
cat cat taa	969
His His	

<210> 60

<211> 984

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF1-AM-SAPORIN

<220>
 <221> CDS
 <222> (1) .. (984)

<400> 60
 aag ccc gtc agc ctg agc tac aga tgc cca tgc cga ttc ttc gaa agc 48
 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1 5 10 15

cat gtt gcc aga gcc aac gtc aag cat ctc aaa att ctc aac act cca 96
 His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
 20 25 30

aac tgt gcc ctt cag att gta gcc cgg ctg aag aac aac aac aga caa 144
 Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
 35 40 45

gtg tgc att gac ccg aag cta aag tgg att cag gag tac ctg gag aaa 192
 Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
 50 55 60

gct tta aac aag agg ttc aag atg gcg atg gtt act agt att acc ctg 240
 Ala Leu Asn Lys Arg Phe Lys Met Ala Met Val Thr Ser Ile Thr Leu
 65 70 75 80

gac ctg gtc aat ccg acc gcc ggc caa tat agc agc ttc gtg gat aag 288
 Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser Ser Phe Val Asp Lys
 85 90 95

att cgt aac aac gta aaa gat ccg aat ctg aaa tac ggt ggt act gat 336
 Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys Tyr Gly Gly Thr Asp
 100 105 110

att gcg gtc atc ggt ccg ccg agc aaa gaa aag ttc ctg cgc att aac 384
 Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys Phe Leu Arg Ile Asn
 115 120 125

ttt caa agc tcc cgt ggc act gtt tct ctg ggc ctg aag cgc gat aac 432
 Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly Leu Lys Arg Asp Asn
 130 135 140

ctg tat gtt gtt gcc tat ctg gcg atg gat aat acg aac gtg aac cgc 480
 Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn Thr Asn Val Asn Arg
 145 150 155 160

gcc tac tac ttt cgt agc gag att acg agc gcg gaa tcc act gct ctg 528
 Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala Glu Ser Thr Ala Leu
 165 170 175

ttc ccg gag gcg acc act gca aac caa aaa gca ctg gaa tat acg gaa 576
 Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu Glu Tyr Thr Glu
 180 185 190

gat tac cag tcc atc gag aag aac gcg cag atc acc cag ggc gat caa 624
 Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr Gln Gly Asp Gln
 195 200 205

tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg ctg agc acg agc atg 672
 Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Ser Thr Ser Met
 210 215 220

gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa gac gaa gcc cgc ttc 720
 Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys Asp Glu Ala Arg Phe
 225 230 235 240

ctg ctg atc gcc att cag atg acg gca gaa gcc gcc cgt ttc cgc tac 768

Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala	Glu	Ala	Ala	Arg	Phe	Arg	Tyr	
				245					250					255		
att	cag	aac	ctg	gtc	atc	aaa	aac	ttc	ccg	aac	aag	ttc	aat	tcc	gag	816
Ile	Gln	Asn	Leu	Val	Ile	Lys	Asn	Phe	Pro	Asn	Lys	Phe	Asn	Ser	Glu	
			260					265					270			
aat	aaa	gtc	att	cag	ttc	gag	gtt	aat	tgg	aaa	aaa	att	tcc	acc	gcc	864
Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Asn	Trp	Lys	Lys	Ile	Ser	Thr	Ala	
		275					280					285				
att	tat	ggg	gac	gcg	aag	aac	ggg	gtt	ttc	aat	aaa	gat	tat	gat	ttt	912
Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	Phe	Asn	Lys	Asp	Tyr	Asp	Phe	
	290					295					300					
ggg	ttc	ggg	aag	gta	cgt	cag	gtg	aaa	gac	ctg	caa	atg	ggg	ctg	ctg	960
Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	Asp	Leu	Gln	Met	Gly	Leu	Leu	
305					310					315					320	
atg	tac	cta	gga	aaa	ccg	aag	taa									984
Met	Tyr	Leu	Gly	Lys	Pro	Lys										
				325												

<210> 61
 <211> 972
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(972)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein EOTAXIN-AM-truncated Shiga-A1 Subunit

<400>	61															
atg	ggg	cca	gct	tct	gtc	cca	acc	acc	tgc	tgc	ttt	aac	ctg	gcc	aat	48
Met	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys	Cys	Phe	Asn	Leu	Ala	Asn	
1				5					10					15		
agg	aag	ata	ccc	ctt	cag	cga	cta	gag	agc	tac	agg	aga	atc	acc	agt	96
Arg	Lys	Ile	Pro	Leu	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Ile	Thr	Ser	
			20					25					30			
ggc	aaa	tgt	ccc	cag	aaa	gct	gtg	atc	ttc	aag	acc	aaa	ctg	gcc	aag	144
Gly	Lys	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	Ala	Lys	
		35				40						45				
gat	atc	tgt	gcc	gac	ccc	aag	aag	aag	tgg	gtg	cag	gat	tcc	atg	aag	192
Asp	Ile	Cys	Ala	Asp	Pro	Lys	Lys	Lys	Trp	Val	Gln	Asp	Ser	Met	Lys	
	50					55					60					
tat	ctg	gac	caa	aaa	tct	cca	act	cca	aag	cca	gcg	atg	aaa	gaa	ttc	240
Tyr	Leu	Asp	Gln	Lys	Ser	Pro	Thr	Pro	Lys	Pro	Ala	Met	Lys	Glu	Phe	
	65				70				75					80		
acc	ctg	gac	ttt	tcc	act	gca	aaa	act	tac	gtc	gat	agc	ctg	aat	gtg	288
Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser	Leu	Asn	Val	
				85					90					95		
att	cgt	tcc	gcg	atc	ggg	acg	ccg	ctg	caa	acg	att	tcc	agc	ggg	ggg	336
Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly	Gly	
			100					105					110			

act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct	384
Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala	
115 120 125	
gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg	432
Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu	
130 135 140	
cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac	480
Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn	
145 150 155 160	
cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg	528
Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr	
165 170 175	
ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct tat act	576
Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr	
180 185 190	
acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat	624
Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn	
195 200 205	
cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat tct ggc	672
Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly	
210 215 220	
acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg	720
Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr	
225 230 235 240	
gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc	768
Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg	
245 250 255	
acc act tta gac gat ctg tct ggc cgc agc tat gtg atg act gcc gaa	816
Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu	
260 265 270	
gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt ctg ccg	864
Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro	
275 280 285	
gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt atc agc ttt ggc	912
Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly	
290 295 300	
tct att aat gcc atc cta ggc tcc gtc gca ctg att ctc aat tgc cac	960
Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His	
305 310 315 320	
cac cac gct taa	972
His His Ala	

<210> 62
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(978)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-

toxin fusion protein EOTAXIN-AM-truncated Shiga-A1 Subunit HIS6

<400> 62
atg ggg cca gct tct gtc cca acc acc tgc tgc ttt aac ctg gcc aat 48
Met Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn
1 5 10 15

agg aag ata ccc ctt cag cga cta gag agc tac agg aga atc acc agt 96
Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser
20 25 30

ggc aaa tgt ccc cag aaa gct gtg atc ttc aag acc aaa ctg gcc aag 144
Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys
35 40 45

gat atc tgt gcc gac ccc aag aag aag tgg gtg cag gat tcc atg aag 192
Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys
50 55 60

tat ctg gac caa aaa tct cca act cca aag cca gcg atg aaa gaa ttc 240
Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro Ala Met Lys Glu Phe
65 70 75 80

acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg 288
Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val
85 90 95

att cgt tcc gcg atc ggt acg ccg ctg caa acg att tcc agc ggt ggt 336
Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly
100 105 110

act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct 384
Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala
115 120 125

gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg 432
Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu
130 135 140

cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac 480
Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn
145 150 155 160

cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg 528
Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr
165 170 175

ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct tat act 576
Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr
180 185 190

acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat 624
Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn
195 200 205

cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat tct ggc 672
Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly
210 215 220

acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg 720
Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr
225 230 235 240

gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc 768
Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg

245										250					255					
acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	gcc	gaa	816				
Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	Ala	Glu					
			260					265					270							
gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggc	ttg	tct	tcc	ggt	ctg	ccg	864					
Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	Leu	Pro					
		275					280					285								
gat	tat	cac	ggc	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	ttt	ggc	912				
Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	Phe	Gly					
	290					295					300									
tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	tgc	cac	960				
Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	Cys	His					
305					310					315					320					
cac	cac	cat	cat	cat	taa											978				
His	His	His	His	His																
				325																

<210> 63
 <211> 993
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) .. (993)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein EOTAXIN-AM-SAPORIN

<400> 63																
atg	ggg	cca	gct	tct	gtc	cca	acc	acc	tgc	tgc	ttt	aac	ctg	gcc	aat	48
Met	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys	Cys	Phe	Asn	Leu	Ala	Asn	
1				5					10					15		
agg	aag	ata	ccc	ctt	cag	cga	cta	gag	agc	tac	agg	aga	atc	acc	agt	96
Arg	Lys	Ile	Pro	Leu	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Ile	Thr	Ser	
			20					25					30			
ggc	aaa	tgt	ccc	cag	aaa	gct	gtg	atc	ttc	aag	acc	aaa	ctg	gcc	aag	144
Gly	Lys	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	Ala	Lys	
		35				40						45				
gat	atc	tgt	gcc	gac	ccc	aag	aag	aag	tgg	gtg	cag	gat	tcc	atg	aag	192
Asp	Ile	Cys	Ala	Asp	Pro	Lys	Lys	Lys	Trp	Val	Gln	Asp	Ser	Met	Lys	
	50					55					60					
tat	ctg	gac	caa	aaa	tct	cca	act	cca	aag	cca	gcg	atg	gtt	act	agt	240
Tyr	Leu	Asp	Gln	Lys	Ser	Pro	Thr	Pro	Lys	Pro	Ala	Met	Val	Thr	Ser	
65					70				75						80	
att	acc	ctg	gac	ctg	gtc	aat	ccg	acc	gcc	ggc	caa	tat	agc	agc	ttc	288
Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	Ser	Phe	
				85					90					95		
gtg	gat	aag	att	cgt	aac	aac	gta	aaa	gat	ccg	aat	ctg	aaa	tac	ggc	336
Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	Tyr	Gly	
			100					105					110			

ggt act gat att gcg gtc atc ggt ccg ccg agc aaa gaa aag ttc ctg	384
Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys Phe Leu	
115 120 125	
cgc att aac ttt caa agc tcc cgt ggc act gtt tct ctg ggc ctg aag	432
Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly Leu Lys	
130 135 140	
cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg gat aat acg aac	480
Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn Thr Asn	
145 150 155 160	
gtg aac cgc gcc tac tac ttt cgt agc gag att acg agc gcg gaa tcc	528
Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala Glu Ser	
165 170 175	
act gct ctg ttc ccg gag gcg acc act gca aac caa aaa gca ctg gaa	576
Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu Glu	
180 185 190	
tat acg gaa gat tac cag tcc atc gag aag aac gcg cag atc acc cag	624
Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr Gln	
195 200 205	
ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg ctg agc	672
Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Ser	
210 215 220	
acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa gac gaa	720
Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys Asp Glu	
225 230 235 240	
gcc cgc ttc ctg ctg atc gcc att cag atg acg gca gaa gcc gcc cgt	768
Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala Ala Arg	
245 250 255	
ttc cgc tac att cag aac ctg gtc atc aaa aac ttc ccg aac aag ttc	816
Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn Lys Phe	
260 265 270	
aat tcc gag aat aaa gtc att cag ttc gag gtt aat tgg aaa aaa att	864
Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys Lys Ile	
275 280 285	
tcc acc gcc att tat ggt gac gcg aag aac ggt gtt ttc aat aaa gat	912
Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp	
290 295 300	
tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa gac ctg caa atg	960
Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met	
305 310 315 320	
ggt ctg ctg atg tac cta gga aaa ccg aag taa	993
Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	
325 330	

<210> 64
 <211> 744
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct encoding
 Methionine-truncated Shiga-A1 Subunit fusion protien

<220>

<221> CDS
 <222> (1) .. (744)

<400> 64

atg	aaa	gaa	ttc	acc	ctg	gac	ttt	tcc	act	gca	aaa	act	tac	gtc	gat	48
Met	Lys	Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	
1				5					10					15		
agc	ctg	aat	gtg	att	cgt	tcc	gcg	atc	ggg	acg	ccg	ctg	caa	acg	att	96
Ser	Leu	Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	
			20					25					30			
tcc	agc	ggg	ggg	act	tcc	ctc	ctg	atg	att	gat	tcc	ggg	acg	ggg	gat	144
Ser	Ser	Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	
		35					40					45				
aac	ttg	ttt	gct	gtt	gat	gtg	cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	192
Asn	Leu	Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	
	50					55					60					
ttt	aat	aat	ctg	cgt	ctg	atc	gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	240
Phe	Asn	Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	
65				70						75					80	
ggg	ttt	gtg	aac	cgt	acg	aac	aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	288
Gly	Phe	Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	
				85					90					95		
tcc	cac	gta	acg	ttt	ccg	ggc	acc	act	gct	gtt	act	ctg	agc	ggc	gat	336
Ser	His	Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	
			100					105					110			
tct	tct	tat	act	acg	tta	cag	cgt	gtg	gct	ggg	atc	agc	cgc	act	ggg	384
Ser	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	
		115					120					125				
atg	caa	atc	aat	cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	432
Met	Gln	Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	
	130					135					140					
agc	cat	tct	ggc	acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	480
Ser	His	Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	
145					150				155						160	
cgc	ttc	gtg	acg	gtc	acc	gcc	gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	528
Arg	Phe	Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	
				165					170					175		
cgc	ggc	ttc	cgc	acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	576
Arg	Gly	Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	
			180					185					190			
atg	act	gcc	gaa	gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggg	cgc	ttg	tct	624
Met	Thr	Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	
		195					200					205				
tcc	gtt	ctg	ccg	gat	tat	cac	ggg	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	672
Ser	Val	Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	
	210					215					220					
atc	agc	ttt	ggc	tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	720
Ile	Ser	Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	
225					230					235					240	
ctc	aat	tgc	cac	cac	cac	gct	taa									744
Leu	Asn	Cys	His	His	His	Ala										
				245												

<210> 65
 <211> 750
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct encoding
 Methionine-truncated Shiga-A1 Subunit HIS6 fusion protein

<220>
 <221> CDS
 <222> (1)..(750)

<400> 65
 atg aaa gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat 48
 Met Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp
 1 5 10 15

agc ctg aat gtg att cgt tcc gcg atc ggt acg ccg ctg caa acg att 96
 Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile
 20 25 30

tcc agc ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat 144
 Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp
 35 40 45

aac ttg ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt 192
 Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg
 50 55 60

ttt aat aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg 240
 Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr
 65 70 75 80

ggt ttt gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc 288
 Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe
 85 90 95

tcc cac gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat 336
 Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp
 100 105 110

tct tct tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt 384
 Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly
 115 120 125

atg caa atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg 432
 Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met
 130 135 140

agc cat tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg 480
 Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu
 145 150 155 160

cgc ttc gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa 528
 Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln
 165 170 175

cgc ggc ttc cgc acc act tta gac gat ctg tct ggc cgc agc tat gtg 576
 Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val
 180 185 190

atg act gcc gaa gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct 624
 Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser
 195 200 205

tcc gtt ctg ccg gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt	672
Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg	
210 215 220	
atc agc ttt ggc tct att aat gcc atc cta ggc tcc gtc gca ctg att	720
Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile	
225 230 235 240	
ctc aat tgc cac cac cac cat cat cat taa	750
Leu Asn Cys His His His His His His	
245 250	

<210> 66
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct encoding
 Methionine-Saporin fusion protein

<220>
 <221> CDS
 <222> (1)..(765)

<400> 66	
atg gtt act agt att acc ctg gac ctg gtc aat ccg acc gcc ggc caa	48
Met Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln	
1 5 10 15	
tat agc agc ttc gtg gat aag att cgt aac aac gta aaa gat ccg aat	96
Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn	
20 25 30	
ctg aaa tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa	144
Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys	
35 40 45	
gaa aag ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct	192
Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser	
50 55 60	
ctg ggc ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg	240
Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met	
65 70 75 80	
gat aat acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg	288
Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr	
85 90 95	
agc gcg gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa	336
Ser Ala Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln	
100 105 110	
aaa gca ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg	384
Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala	
115 120 125	
cag atc acc cag ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att	432
Gln Ile Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile	
130 135 140	
gat ctg ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg	480
Asp Leu Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val	

<220>
 <223> Pseudomonas toxin carboxy-terminal endoplasmic reticulum retention
 signal

<400> 68
 Xaa Asp Glu Leu
 1

<210> 69
 <211> 393
 <212> DNA
 <213> Mus musculus

<220>
 <223> Mouse chemokine ALP cDNA

<220>
 <221> CDS
 <222> (11) .. (373)

<400> 69
 ctgagtgagc atg atg gag ggg ctc tcc ccc gcc agc agc ctc ccg ctg 49
 Met Met Glu Gly Leu Ser Pro Ala Ser Ser Leu Pro Leu
 1 5 10

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 Leu Leu Leu Leu Leu Ser Pro Ala Pro Glu Ala Ala Leu Pro Leu Pro
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 Arg Leu Leu Arg Arg Ile Val His Met Glu Leu Gln Glu Ala Asp Gly
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 Asp Cys His Leu Gln Ala Val Val Leu His Leu Ala Arg Arg Ser Val
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 Cys Val His Pro Gln Asn Arg Ser Leu Ala Arg Trp Leu Glu Arg Gln
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 Gly Lys Arg Leu Gln Gly Thr Val Pro Ser Leu Asn Leu Val Leu Gln
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Met Val Ile Phe Glu Thr Ile Tyr Cys Asn Arg Lys Glu Val Ile Ala
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Val Pro Lys Asn Gly Ser Met Ile Cys Leu Asp Pro Asp Ala Pro Trp
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Val Lys Ala Thr Val Gly Pro Ile Thr Asn Arg Phe Leu Pro Glu Asp
85 90 95

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Leu Lys Gln Lys Glu Phe Pro Pro Ala Met Lys Leu Leu Tyr Ser Val
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Glu His Glu Lys Pro Leu Tyr Leu Ser Phe Gly Arg Pro Glu Asn Lys
115 120 125

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Arg Ile Phe Pro Phe Pro Ile Arg Glu Thr Ser Arg His Phe Ala Asp
130 135 140

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Leu Ala His Asn Ser Asp Arg Asn Phe Leu Arg Asp Ser Ser Glu Val
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